

## EXHIBIT E

ClustalW (v1.4) multiple sequence alignment

```

huLGR8-B      1 MIVFLVFKHLFSLRLITMFFLLHFIVLINVKDFALTQGSMITPSCQKGYF  50
huLGR8-B_N    1                                     QGSMITPSCQKGYF  14
                                     *****

huLGR8-B      51 PCGNLTKCLPRAFHCDGKDDCGNGADEENCGDTSGWATIFGTVHGNANSV 100
huLGR8-B_N    15 PCGNLTKCLPRAFHCDGKDDCGNGADEENCGDTSGWATIFGTVHGNANSV  64
               *****

huLGR8-B      101 ALTQECFLKQYPQCCDCKETELECVDLKSVPMSISNNVTLLSLKKNKIH 150
huLGR8-B_N    65 ALTQECFLKQYPQCCDCKETELECVDLKSVPMSISNNVTLLSLKKNKIH 114
               *****

huLGR8-B      151 SLPDKVFIKYTKLKKIFLQHNCIRHISRKAFFGLCNLQILYLNHNCITT 200
huLGR8-B_N    115 SLPDKVFIKYTKLKKIFLQHNCIRHISRKAFFGLCNLQILYLNHNCITT 164
               *****

huLGR8-B      201 RPGIFKDLHQLTWLILDDNPITRISQRLFTGLNSLFFLSMVNNYLEALPK 250
huLGR8-B_N    165 RPGIFKDLHQLTWLILDDNPITRISQRLFTGLNSLFFLSMVNNYLEALPK 214
               *****

huLGR8-B      251 QMCAQMPQLNWVDLEGNRIKYLTNSTFLSCDSLTVLDLSSNTITELSPHL 300
huLGR8-B_N    215 QMCAQMPQLNWVDLEGNRIKYLTNSTFLSCDSLTVLDLSSNTITELSPHL 264
               *****

huLGR8-B      301 FKDLKLLQKLNLSNPLMYLHKNQFESLKQLQSLDLERIEIPNINTRMFQ 350
huLGR8-B_N    265 FKDLKLLQKLNLSNPLMYLHKNQFESLKQLQSLDLERIEIPNINTRMFQ 314
               *****

huLGR8-B      351 PMKNLSHIYFKNFRYCSYAPHVRICMPLTDGISSFEDLLANNILRIFVWV 400
huLGR8-B_N    315 PMKNLSHIYFKNFRYCSYAPHVRICMPLTDGISSFEDLLANNILR 359
               *****

huLGR8-B      401 IAFITCFGNLFFVIGMRSFIKAENTTHAMSIKILCCADCLMGVYLFFVGIF 450
huLGR8-B_N    360                                     359

huLGR8-B      451 DIKYRGQYQKYALLWMESVQCRLMGFLAMLSTEVSVLLLTLYLTLEKFLVI 500
huLGR8-B_N    360                                     359

huLGR8-B      501 VFPSNIRPGKRQTSVILICIWMAGFLIAVIPFWNKDYFGNFYKNGVCF 550
huLGR8-B_N    360                                     359

huLGR8-B      551 PLYYDQTEDIGSKGYSLGIFLGVNLLAFLIIVFSYITMFCSIQKTALQTT 600
huLGR8-B_N    360                                     359

huLGR8-B      601 EVRNCFGREVAVANRFFFIVFSDAICWIPVFVVKILSLFRVEIPDTMTSW 650
huLGR8-B_N    360                                     359

```

huLGR8-B 651 IVIFFLPVNSALNPILYTLTTNFFKDKLKQLLHKHQKRSIFKIKKKSLST 700  
huLGR8-B\_N 360 359

huLGR8-B 701 SIVWIEDSSSLKLGVLNKITLGDSIMKPVS 730  
huLGR8-B\_N 360 359